AMENDMENTS TO THE CLAIMS

1-16. **(Canceled)**

17. **(Previously Presented)** A diagnostic hearing loss microarray comprising at least 5 sequences that are indicative of presence or absence of an allele associated with a risk for hearing loss, wherein said sequences are selected from the group consisting of genetic sequences from CDH23, MYO7A, OTOF, SLC26A4 and USH2A.

18. **(Original)** The microarray of Claim 17, wherein said sequences comprise multiple adjacent exons.

19. **(Previously Presented)** The microarray of Claim 18, wherein said multiple adjacent exons are selected from the group comprising CDH23 exons 2-3, CDH23 exons 4-6, CDH23 exons 7-9, CDH23 exons 10-11, CDH23 exons 12-13, CDH23 exons 14-16, CDH23 exons 17-21, CDH23 exons 22-27, CDH23 exons 28-31, CDH23 exons 32-36, CDH23 exons 37-43, CDH23 exons 44-46, CDH23 exons 47-53, CDH23 exons 53-68, MYO7A exons 5-14, MYO7A exons 16-21, MYO7A exons 16-18, MYO7A exons 22-26, MYO7A exons 28-35, MYO7A exons 36-44, MYO7A exons 45-49, OTOF exons 4-5, OTOF exons 6-8, OTOF exons 9-11, OTOF exons 12-25, OTOF exons 16-25, OTOF exons 16-18, OTOF exons 16-20, OTOF exons 19-20, OTOF exons 21-25, OTOF exons 16-39, OTOF exons 26-39, OTOF exons 40-47, SLC26A4 exons 1-3, SLC26A4 exons 4-6, SLC26A4 exons 11-18, SLC26A4 exons 19-21, USH2A exons 1-3, USH2A exons 5-9, USH2A exons 10-11, USH2A exons 12-13, USH2A exons 15-16 and USH2A exons 17-20.

20. **(Original)** The microarray of Claim 17, wherein said sequences comprise a single exon.

21. **(Previously Presented)** The microarray of Claim 20, wherein said single exon is selected from the group consisting of MYO7A exon 1, MYO7A exon 2, MYO7A exon 3, MYO7A exon 4, MYO7A exon 15, MYO7A exon 21, MYO7A exon 27, OTOF exon 1, OTOF exon 2, OTOF exon 3, USH2A exon 4, USH2A exon 14 and USH2A exon 21.

22. **(Original)** A kit for detecting a candidate gene responsible for hearing loss comprising:

a microarray of Claim 17; and

buffers and components to be used with said microarray.

23. **(Original)** The kit of Claim 22, wherein the microarray comprises a solid support comprising a plurality of capture nucleotide sequences bound to the solid support, wherein said capture nucleotide sequences are representative of regions of candidate genes for hearing loss, and wherein the support of the kit is adapted to be contacted with a sample from a patient comprising target nucleic acid sequences, and wherein the contacting permits hybridization under stringent conditions of a target nucleic acid sequence and a capture nucleotide sequence representative of regions of candidate genes for hearing loss.

24. **(Canceled)**